CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/914,151   **ENTERED**

CRF Processing Date: 10/3/2001
Edited by: _____
Verified by: _____ (STIC sta[

KW

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

  _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

  _____

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

  _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

  _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

  _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

  _____

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:

  _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

  _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: *aligned amino acid nos. in Seq. 1*

  _____

  _____

  _____

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                    RAW SEQUENCE LISTING              DATE: 10/03/2001
                    PATENT APPLICATION:  US/09/914,151   TIME: 17:10:09

                    Input Set : A:\pto.txt
                    Output Set: N:\CRF3\10032001\I914151.raw


       3 <110> APPLICANT: Juridical Foundation, Japanese Foundation For Cancer Research
       5 <120> TITLE OF INVENTION: vector for gene therapy of malignant melanoma, with use of
virus h
       6        aving MSH fused protein.
       8 <130> FILE REFERENCE: H11-0241J2
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/914,151
C--> 10 <141> CURRENT FILING DATE: 2001-08-24
      10 <160> NUMBER OF SEQ ID NOS: 39
      12 <170> SOFTWARE: PatentIn Ver. 2.0
      14 <210> SEQ ID NO: 1
      15 <211> LENGTH: 166
      16 <212> TYPE: DNA
      17 <213> ORGANISM: Artificial Sequence
      19 <220> FEATURE:
      20 <223> OTHER INFORMATION: DNA coding a part of adenovirus type 5 fiber, AS linker
peptide an
      21        d Y-MSH.
      23 <220> FEATURE:
      24 <221> NAME/KEY: CDS
      25 <222> LOCATION: (3)..(113)
      27 <400> SEQUENCE: 1
      28   gg gaa ttc tcg agt tac act ttt tca tac att gcc caa gaa cca tca        47
      29      Glu Phe Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu Pro Ser
      30       1               5                  10                  15
      31   gcc tcc gca tct gct tcc gcc cct gga tcc tac tcc atg gag cac ttc        95
      32   Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Tyr Ser Met Glu His Phe
      33                 20                  25                  30
      34   cgc tgg ggc aag ccg gtg taaagaatcg tttgtgttat gtttcaacgt        143
      35   Arg Trp Gly Lys Pro Val
      36                 35
      37   gtttattttt caattgaatt ccc                                            166
      40 <210> SEQ ID NO: 2
      41 <211> LENGTH: 126
      42 <212> TYPE: DNA
      43 <213> ORGANISM: Artificial Sequence
      45 <220> FEATURE:
      46 <223> OTHER INFORMATION: synthetic DNA No.924 used as template for PCR amplification
of DNA
      47        sequence No.1.
      49 <400> SEQUENCE: 2
      50   cgttgaaaca taacacaaac gattctttac accggcttgc cccagcggaa gtgctccatg        60
      51   gagtaggatc caggggcgga agcagatgcg gaggctgatg gttcttgggc aatgtatgaa       120
      52   aaagtg                                                               126
      55 <210> SEQ ID NO: 3
      56 <211> LENGTH: 39
      57 <212> TYPE: DNA
      58 <213> ORGANISM: Artificial Sequence
      60 <220> FEATURE:
      61 <223> OTHER INFORMATION: synthetic DNA No.933 used as sense primer for PCR
amplification of
      62        DNA sequence No.1.
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 64 <400> SEQUENCE: 3
 65   gggaattctc gagttacact ttttcataca ttgcccaag                    39
 68 <210> SEQ ID NO: 4
 69 <211> LENGTH: 49
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:
 74 <223> OTHER INFORMATION: synthetic DNA No.934 used as antisense primer for PCR
amplification
 75      of DNA sequence No.1.
 77 <400> SEQUENCE: 4
 78   gggaattcaa ttgaaaaata aacacgttga aacataacac aaacgattc           49
 81 <210> SEQ ID NO: 5
 82 <211> LENGTH: 76
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Artificial Sequence
 86 <220> FEATURE:
 87 <223> OTHER INFORMATION: synthetic DNA No.1061 used as sense primer for PCR
amplification of
 88      DNA coding Y"-MSH and adenovirus fiber poly A signal.
 90 <400> SEQUENCE: 5
 91   cgggatccta ctccatggag cacttccgct ggggcaagcc ggtgtaagtc gacaagaata   60
 92   aagaatcgtt tgtgtt                                                76
 94 <210> SEQ ID NO: 6
 95 <211> LENGTH: 32
 96 <212> TYPE: DNA
 97 <213> ORGANISM: Artificial Sequence
 99 <220> FEATURE:
100 <223> OTHER INFORMATION: synthetic DNA No.1092 used as antisense primer for PCR
amplificati
101      on of DNA coding Y"-MSH and adenovirus fiber poly A signal.
103 <400> SEQUENCE: 6
104   cggaattcat ggcgccatgt ttaatcagag gt                             32
107 <210> SEQ ID NO: 7
108 <211> LENGTH: 1818
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: DNA coding a modified fiber protein of pWE6.7R-F/asMSHa
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (1)..(1815)
119 <400> SEQUENCE: 7
120   atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48
121   Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
122    1               5                  10                  15
124   tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
125   Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
126                  20                  25                  30
128   ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  144
129   Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
130                  35                  40                  45
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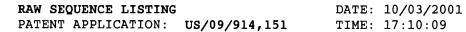
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132   ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
133   Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
134       50                  55                  60
136   aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
137   Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
138    65                  70                  75                  80
140   caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
141   Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
142                   85                  90                  95
144   ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
145   Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
146                  100                 105                 110
148   act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
149   Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
150                  115                 120                 125
152   atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
153   Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
154       130                 135                 140
156   gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
157   Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
158   145                 150                 155                 160
160   aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
161   Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
162                  165                 170                 175
164   gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
165   Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
166                  180                 185                 190
168   aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
169   Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
170       195                 200                 205
172   gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
173   Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
174       210                 215                 220
176   ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   720
177   Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
178   225                 230                 235                 240
180   gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   768
181   Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
182                  245                 250                 255
184   gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   816
185   Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
186       260                 265                 270
188   agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
189   Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
190       275                 280                 285
192   ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
193   Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
194       290                 295                 300
196   aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
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197   Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
198   305                 310                 315                 320
200   gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
201   Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
202                   325                 330                 335
204   gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
205   Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
206                   340                 345                 350
208   aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
209   Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
210                   355                 360                 365
212   tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
213   Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
214                   370                 375                 380
216   agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
217   Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
218   385                 390                 395                 400
220   ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
221   Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
222                   405                 410                 415
224   aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
225   Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
226                   420                 425                 430
228   ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
229   Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
230                   435                 440                 445
232   tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
233   Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
234                   450                 455                 460
236   gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
237   Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
238   465                 470                 475                 480
240   aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
241   Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
242                   485                 490                 495
244   ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
245   Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
246                   500                 505                 510
248   aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
249   Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
250                   515                 520                 525
252   cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632
253   Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
254                   530                 535                 540
256   aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1680
257   Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
258   545                 550                 555                 560
260   cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca   1728
261   His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
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262                    565                570                575
264    tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga    1776
265    Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly
266                    580                585                590
268    tcc tac tcc atg gag cac ttc cgc tgg ggc aag ccg gtg taa          1818
269    Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val
270    '          595                600                605
273 <210> SEQ ID NO: 8
274 <211> LENGTH: 40
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: synthetic DNA No.1037 used as sense primer for PCR
amplification of
280        DNA coding human MSH receptor residue 1-154.
282 <400> SEQUENCE: 8
283    gggaattcac catggctgtg cagggatccc agagaagact                         40
286 <210> SEQ ID NO: 9
287 <211> LENGTH: 33
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: synthetic DNA No.1038 used as antisense primer for PCR
amplification
293        of DNA coding human MSH receptor residue 150-317.
295 <400> SEQUENCE: 9
296    gggaattcac caggagcatg tcagcacctc ctt                               33
299 <210> SEQ ID NO: 10
300 <211> LENGTH: 27
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: synthetic DNA No.1039 used as sense primer for PCR
amplification of
306        DNA coding human MSH receptor residue 150-317.
308 <400> SEQUENCE: 10
309    ctgcggtacc acagcatcgt gaccctg                                      27
311 <210> SEQ ID NO: 11
312 <211> LENGTH: 27
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: synthetic DNA No.1040 used as antisense primer for PCR
amplification
318        of DNA coding human MSH receptor residue 1-154.
320 <400> SEQUENCE: 11
321    gctgtggtac cgcagtgcgt agaagat                                      27
324 <210> SEQ ID NO: 12
325 <211> LENGTH: 107
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: synthetic DNA No.1075 used as sense primer for PCR
```

amplification of

VERIFICATION SUMMARY   DATE: 10/03/2001
PATENT APPLICATION: US/09/914,151   TIME: 17:10:10

Input Set : **A:\pto.txt**
Output Set: **N:\CRF3\10032001\I914151.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date